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Fig. 1

HTRAM.DNA	1	ATGGCGATTG	10	GCAGAGAAAG	20	CACCAAGAGG	30	CCCCCAGTGG	40	TCAGCCACGA	50
KIAA0057.DNA	1	ATGGCTTTCC		GCAAGAGGA-		--GAAAGT		TACCCGCTCT		TCAGCCACGA	50
HWAR1.DNA	1	ATGGGGCTCC		GTAAAGAGAG		CACCAAGAGC		CCCCCGGTTC		TCAGCCACGA	50
RWAR1.DNA	1	ATGGGGCTCC		GCAAGAGAGG		CCCAAGGAGC		CCCCCGGTGG		TCAGCCACGA	50
			60		70		80		90		100
HTRAM.DNA	51	ATTCTGTCCTG		CAGAAACACG		CGGACATCGT		CTCCTGTGTG		GGCATGTTCT	100
KIAA0057.DNA	51	GTTCGTGATC		CACAAACATG		CGGACATCGG		CTTCTGCCCTG		GTGCTCTGGG	100
HWAR1.DNA	51	ATTCTATCCTG		CAGAAACATG		CGGACATCGT		CTCCTGCGGTG		GGCATGTTCT	100
RWAR1.DNA	51	ATTCTATGTTG		CAGAAACACG		CGGATATGGT		CTCCTGCGGTG		GGCATGTTCT	100
			110		120		130		140		150
HTRAM.DNA	101	TCCTGCTGGG		GCTCATGTTT		GAGATACGGG		CAAAAGCTTC		TATCATTTTT	150
KIAA0057.DNA	101	TCCTCATTCGG		GCTTATGTTT		GAGGTACAGC		CAAAAGCTTC		CTTCTTATTT	150
HWAR1.DNA	101	TCCTGCTGGG		GCTTGTGTTG		GAGGTACAGC		CAAAAGCTTC		CATCGTGTTC	150
RWAR1.DNA	101	TCGTGCTGGG		ACTTATGTTT		GAGGTACAGC		CCCAAGCTTC		GATCGTGTTC	150
			160		170		180		190		200
HTRAM.DNA	151	GTACTCTCTC		AGTACATGTT		CACCTCCGCA		GCAACAGAGG		AACAAGCTTC	200
KIAA0057.DNA	151	ATTTTACCTC		AGTATACAT		TAGCTGCCCT		ACAGCAGA--		-----CAG	200
HWAR1.DNA	151	CTCACTCTCTC		AGTACATGTT		TCTGTGCCCT		GCAGCAGAGG		AACAAGCTTC	200
RWAR1.DNA	151	CTCACCTCTC		AGCATGAGTT		CGTTGTCCC-		--AGCAGAG		GGCTACCTTC	200
			210		220		230		240		250
HTRAM.DNA	201	TGAATCAGTG		TCCCTTTTAT		ACTATGGCAT		CAAAAGTTTG		GCTACTGTTT	250
KIAA0057.DNA	201	TGAGACCGTG		---CACTACC		ACTATGGCC		TAAAGACCTG		GTACACATCT	250
HWAR1.DNA	201	GGGTCGAAG		TCCCTCTATT		ATTATGGTGT		CAAAAGTTTG		GCCACGGTTT	250
RWAR1.DNA	201	GGGTCACAG		ACCTTTTACC		ATTATGGGGT		CAAAAGTTTG		GCCACAGTCT	250
			260		270		280		290		300
HTRAM.DNA	251	TCTTCTACAT		GCTAGTGGGG		ATAATTATTC		ATGCCGTAAT		TCAAGAGTAT	300
KIAA0057.DNA	251	TGTTCTACAT		CTTCATCACC		ATCATCTTGC		ATGGTGTGGT		TCAGGAGTAC	300
HWAR1.DNA	251	TCTTCTACAT		GCTGGTGGGA		ATCATTATTC		ATGCCACAAI		TCAGGAGTAT	300
RWAR1.DNA	251	TCTTCTACAT		GCTGGTGGCC		ATCATCATTC		ACGGCACCAT		TCAGGAGTAC	300
			310		320		330		340		350

Fig. 1 (cont.)

HTRAM. DNA	301	ATGTTGGATA	AAATTAACAG	GCGAATGCAC	TCTCCAAAA	CAAAACACAG	350
KIAA0057. DNA	301	ATTTTAGATA	AAATCAGCAA	ACGGCTTCAT	CTCTCCAAAG	TCAAACACAG	350
HWAR1. DNA	301	GTGTTGGATA	AAATTAACAA	GAGAATGCAG	TTCAACAAAG	CGAAACAAAA	350
RWAR1. DNA	301	GTGCTAGATA	AGCTCAGCCG	GAGACTGCAG	CTCAACAAAG	GCAAAACAAA	350
HTRAM. DNA	351	CAAGTTTAAT	GAACTCTGGTC	AGCTTAGTGC	GTTCCTACCTT	TTTGGCTGTG	400
KIAA0057. DNA	351	CAAGTTCAAT	GAATCTGGAC	AGCTGGTCGT	CTTTCATTTTC	ACCTGGGTGA	400
HWAR1. DNA	351	CAAGTTTAAC	GAGTCTGGTC	AGTTTAGTGT	GTTCCTACCTT	TTTTCCTGTA	400
RWAR1. DNA	351	CAAAATTGAAT	GAGGCCGGGC	AGCTCAGTGT	GTTCCTACATA	GTCTCTCGTA	400
HTRAM. DNA	401	TTTGGGGCAC	ATTCAATCTTC	ATCTCTGAAA	ACTACATCTTC	AGACCCCAACT	450
KIAA0057. DNA	401	TTTGGTGCCT	CTACCTGGTG	GTGACCGAAG	GATACCTTAAC	AAACCCAAAG	450
HWAR1. DNA	401	TTTGGGGCAC	ATTCATTTTA	ATCTCTGAAA	ACTGCCCTGTC	AGACCCCAACT	450
RWAR1. DNA	401	TC TGGGGTAT	GATCAATCTG	GCCTCTGAGA	ACTGCCCTGTC	AGACCCCAACT	450
HTRAM. DNA	451	ATCTTATGGA	GGGCTTATCC	CCATAACCTG	ATGACATTTTC	AAATGAAGTT	500
KIAA0057. DNA	451	AGCCTCTGGG	AAGACTACCC	GCATGTGCAC	CTCCCTCTCC	AGGTGAAGTT	500
HWAR1. DNA	451	CTTATATGGA	AGGCTCGTCC	CCATACCATG	ATGACATTTTC	AAATGAAGTT	500
RWAR1. DNA	451	CTATTGTGGA	AGTCTCAGCC	CCACAACATG	ATGACATTTTC	AGATGAAGTT	500
HTRAM. DNA	501	TTTCTACATA	TCA CAGCTGG	CTTACTGGGT	TCATGCTTTT	CCTGAACCTC	550
KIAA0057. DNA	501	TTTCTACATA	TGC CAGCTGG	CTTACTGGGT	GCACGCACCT	CCTGAGCTAT	550
HWAR1. DNA	501	TTTCTACATA	TCC CAGT TGG	CTTACTGGGT	TCATGCTTTT	CCTGAACCTC	550
RWAR1. DNA	501	TTTCTACATC	TCA CAGT TGG	CTTACTGGGT	TCATGCTTTT	CCCGAGCTCT	550



Fig. 1 (cont.)

HTRAM.DNA	551	ACTTCCAGAA	AACCAAAA	GAAGAVATTC	CTCGTCAGCT	TGCTACACAT	600
KIAA0057.DNA	551	ACTTCCAGAA	GGTACGGAAG	GAGGAAATTC	CCGGCCAGCT	CCAGTATATTT	600
HWAR1.DNA	551	ACTTCCAGAA	AACCAAAA	CAAGCATCC	CTCGTCAGCT	TGCTACACAT	600
RWAR1.DNA	551	ACTTCCAGAA	AGTCAGGAAA	CAAGAVATCC	CGGCTCAACT	CATCTACACAT	600
HTRAM.DNA	601	GGTCTTTACC	TCTTCCACAT	TGCTGGAGCT	TACCTTTTGA	ACTTGAATCA	650
KIAA0057.DNA	601	TGCCTGTACC	TGGTGCATAT	AGCTGGAGCA	TACCTCTTAA	ACCTGAGCCG	650
HWAR1.DNA	601	GGTCTTACC	TCTTCCACAT	TACTGGAGCT	TATCTCTTGT	ACTTGAATCA	650
RWAR1.DNA	601	GGCTTCCACC	TCTTCCACAT	TGAGGGGGCC	TATCTCTTGT	ACTTGAACCA	650
HTRAM.DNA	651	TCTAGGACTT	GTCTTCTGG	TGCTACATTA	TTTGTGTGA	TTTCTTTTCC	700
KIAA0057.DNA	651	CCTGGGCCCTG	ATCTTCTGTC	TGCTGCAGTA	CTCAACTGAG	TTCTCTTCC	700
HWAR1.DNA	651	TTTGGGACTT	CTTCTTTTGG	TACTGCATTA	TTTGTGTGA	TTTCTTTTCC	700
RWAR1.DNA	651	CCTGGGCCCTG	CTGCTTCTGA	TGCTGCAGTA	TGCTGTGAG	CTCTCTTCCA	700
HTRAM.DNA	701	ACATTTCCCG	CCTGTTTTAT	TTTAGCAATG	AAAAAGTATCA	GAAAGGATTT	750
KIAA0057.DNA	701	ACACGGCTAG	ACTCTTCTAC	TTTGCAGATG	AAAAACAACGA	GAAACTGTTC	750
HWAR1.DNA	701	ACATGTGCGG	CCTGTTTTAC	TTTAGTATG	AAAAAGTACCA	GAAAGGCAAT	750
RWAR1.DNA	701	CGGTGTGCAG	CCTGCTTTAC	TTTGGGATG	AGCGTACCA	GAAAGGGTTG	750
HTRAM.DNA	751	TCTCTGTGGG	CAGTTCTTTT	TGTTTTGGGA	AGACTTCTGA	CTTTAATTTCT	800
KIAA0057.DNA	751	AGTGCCTGGG	CTGCTGTTTT	TGGGTATACC	CGCTCTTCA	TCTTCACTCT	800
HWAR1.DNA	751	TCTCTGTGGG	CCATTGTGTT	TATCTTGGGT	AGACTTGTGA	CTTTAATTTCT	800
RWAR1.DNA	751	TCTTTGTGGC	CTATCTGTGTT	TATATCCGGG	AGACTCTGTA	CACTGATTTCT	800
HTRAM.DNA	801	TTTCACTACTG	ACTGTTGGTT	TTTGGGCTTGC	AAGACGAGAA	AATCAGAAAC	850
KIAA0057.DNA	801	TGCGGTGCTG	GCATTTGGCT	TTGGACTGGC	TGCTATGGAA	AACAGGCAAT	850
HWAR1.DNA	801	TTCCGTACTC	ACTGTTGGGT	TTTCACTTGGC	TGGATGGCAG	AATCGGAATC	850
RWAR1.DNA	801	CTCAGTGGTT	ACAGTAGGGC	TTTCACTTGGC	CGGAGCA---	AATCGGAATG	850



Fig. 1 (cont.)

HTRAM.DNA	851	TGGATTTCAG	TACTGGAAC	TCAATGTGT	TAGCTGTTAG	AATCGCTGTT	900
KIAA0057.DNA	851	TTGATCCCGA	GAAAGGAAAC	TTCAACACTTT	TGTTTTCAG	GCTCTGCGTG	900
HWAR1.DNA	851	CTGATGCCCT	TACTGGAAT	GTAATGTGT	TGGCAGCTAA	AAATGCTGTT	900
RWAR1.DNA	851	GAAATGCTCT	CTCTGTTAT	GTCATGTGT	TGGCAGCTAA	AAATGCTGTT	900
		910	920	930	940	950	
HTRAM.DNA	901	CTGGCATCCA	TTTGGCTTAC	TCAGGCAATT	ATCATGTGGA	AGTTCAATTA	950
KIAA0057.DNA	901	CTCTCTGG	TCTGTCCGC	CCAGGCTGG	CTCATGTGGC	GCTTCATCCA	950
HWAR1.DNA	901	CTGTGCTCCA	CTTGCACCAT	CCAPCCCTAC	GTAACATGGA	ACTTAATTAC	950
RWAR1.DNA	901	CTGTCTCTCA	CTTGCAGTAT	CCAGCTGTAC	ATAACATGGA	CCTTGACGAC	950
		960	970	980	990	1000	
HTRAM.DNA	951	TTTTCAGCTT	CGAAGGTGGA	GGGAACATTC	TGCTTTTCAG	-GCACAGCTT	1000
KIAA0057.DNA	951	CTCCAGCTG	CGGCACCTGC	GGGAATCTTG	GAATGAGCAG	AGTGCAAGGC	1000
HWAR1.DNA	951	TCTCTGGCTT	CAGAGGTGG	TAGAAGATTC	TAATATTCAG	-GCCATCATGT	1000
RWAR1.DNA	951	CGTCTGGCTT	CAGAGATGCT	TAGAAGATTC	GAATCTTCAT	-GTCCT---GT	1000
		1010	1020	1030	1040	1050	
HTRAM.DNA	1001	GTGAAGAAGA	AACCA-ACAG	TACATA-AG	GCAGATCTTC	TAAAAAAGGA	1050
KIAA0057.DNA	1001	GGAGAGTCCC	AGCCACACCC	AGACTACAG	CCAGGCTCAT	CAAGAGGGA	1050
HWAR1.DNA	1001	ATGAAAGA	AAC-----GG	TCG-----	--AGATCTTC	TAAAAAAGA	1050
RWAR1.DNA	1001	GGAGGAAGA	GAC-----GG	TC-----	-CAGGTC---	GAGAAAAGGC	1050
		1060	1070	1080	1090	1100	
HTRAM.DNA	1051	ACAGAAATG	GTGTGAATGG	BACATTAAC	TCAAATGTAG	CAGACTCTCC	1100
KIAA0057.DNA	1051	TCTGTTACC	ATGAAATGG	AGTGGTGAAG	CCAGAGACAG	GACCTCTCC	1100
HWAR1.DNA	1051	ACAGAAACG	GAGTG---GG	AGTGGAACT	TCAAATAGAG	TAGACTGTCC	1100
RWAR1.DNA	1051	ACAGAAATG	GAGTGCA--G	AA-----T	CCAAATAGAA	TAGATCTCTCC	1100
		1110	1120	1130	1140	1150	
HTRAM.DNA	1101	CCGGAATAAA	AAAGAGAAAT	CTTCA.....	.....	.....	1150
KIAA0057.DNA	1101	ACGCACTAAG	AAACTCAAGT	CTCCC.....	.....	.....	1150
HWAR1.DNA	1101	GCCTAAGAGC	AAAGAGAAAT	CTTCA.....	.....	.....	1150
RWAR1.DNA	1101	ACCAAGCAAG	AAAGAGAAAG	CTCCT.....	.....	.....	1150



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Fig. 2

HTRAM.AMI	1	MAIRKKSTKS	10	PPVLSHEEVL	20	QNHADIVSCV	30	AMVLLGLME	40	EITAKASTIE	50
KIAA0057.AMI	1	MAFRRR-TKS	YELFSQEEVI	HNHADIGFCL	QNHADIVSCV	GMFEFLGLVE	GMFEFLGLME	90	100	EVTAKTAFLE	50
HWAR1.AMI	1	MGLRKKSTKN	PPVLSQEEIL	QNHADIVSCV	GMFEFLGLVE	GMFEFLGLME	90	100	EGTAESIVE	50	
RWAR1.AMI	1	MGLRKKNARN	PPVLSHEEVL	QNHADIVSCV	GMFEFLGLVE	GMFEFLGLME	90	100	EGTAESIVE	50	
HTRAM.AMI	51	VTLCYNVTLE	ATEBOATESV	SLYYYGKIKDL	ATVFFVYMLVA	IIIIHAVIQEY	100	100	IIIIHAVIQEY	100	
KIAA0057.AMI	51	ILPCYNISVE	TADSETVH--	--YHYGPKDL	VTILEYIFIT	IIIIHAVIQEY	100	100	IIIIHAVIQEY	100	
HWAR1.AMI	51	LTLCQSVAVE	AAEEQATGSK	SLYYYGKIKDL	ATVFFVYMLVA	IIIIHAVIQEY	100	100	IIIIHAVIQEY	100	
RWAR1.AMI	51	LTLCQGVWVE	A-ELPSGSR	TLYHYGVKDL	ATVFFVYMLVA	IIIIHAVIQEY	100	100	IIIIHAVIQEY	100	
HTRAM.AMI	101	MLDKINRRMH	FSKTKHSKEN	ESGQLSAEYL	EAQVWGTFIL	ISENYISDPT	150	150	ISENYISDPT	150	
KIAA0057.AMI	101	ILDKISKRLH	LSKVHSHKEN	ESGQLVVEHF	TSVIMCFYV	VTGYLTNER	150	150	VTGYLTNER	150	
HWAR1.AMI	101	VLDKINKRMQ	FTKAKQNKEN	ESGQFSVEYE	FSCINGTFIL	ISENCLSDPT	150	150	ISENCLSDPT	150	
RWAR1.AMI	101	VLDKLSRRLQ	LTKGQNKLN	EAGQLSVEYI	VSGIWMGITL	ASENCLSDPT	150	150	ASENCLSDPT	150	
HTRAM.AMI	151	ILWRAYPHNL	MTEQMKFEYI	SQLAYWLHAF	PELYFQKTKK	EDIPROLVYI	200	200	EDIPROLVYI	200	
KIAA0057.AMI	151	SLWEDYPHVH	LPEQVKFEYL	CQLAYWLHAL	PELYFQKVRK	EEIPROLQYI	200	200	EEIPROLQYI	200	
HWAR1.AMI	151	LIWKARPHSM	MTEQMKFEYI	SQLAYWFHAF	PELYFQKTKK	QDIPROLVYI	200	200	QDIPROLVYI	200	
RWAR1.AMI	151	LLWKSQPHNM	MTEQMKFEYI	SQLAYWFHSE	PELYFQKVRK	QDIPROLVYI	200	200	QDIPROLVYI	200	



Fig. 2 (cont.)

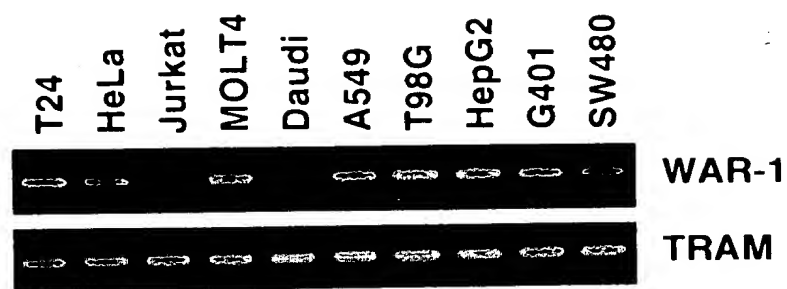
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HWAR1.AMI	201	GLHLEHIITGA	YLLIYNHIGL	LLVLHYEVE	LISHMCGLFY	ESDEKYOKGI	250
RWAR1.AMI	201	GLHLEHIIGGA	YLLIYNHIGL	LLIMLHYAVE	LSSVCSLILY	EGDERYOKGL	250
			270	280	290	300	
HTRAM.AMI	251	SIMAVLEVLG	RLLTLLLSVL	TVGEGTARAE	NOKLDFSTGN	FNVLAURIIV	300
KIAA0057.AMI	251	SAMAAVEGVT	RLFILTLAVI	AIGEGTARME	NOAFPEKGN	FNTLFCRLQV	300
HWAR1.AMI	251	SLWAIIVFILG	RLVTLIVSVL	TVGEGHLAGSQ	NRNPDAITGN	VNVLAAKIAV	300
RWAR1.AMI	251	SIMPIVEFISC	RLVTLIVSVV	TVGLHLTAGT-	NRNGNALSGN	VNVLAAKIAV	300
			310	330	340	350	
HTRAM.AMI	301	LASICVTQAF	MMWKFINFQL	RWRREHSAFO	APAVKKKPTV	TK--GRSSKK	350
KIAA0057.AMI	301	LLLVCAAQAM	LMWRFFHSQL	RHWREYWN-E	QSAKRRRVFAT	PRLPARLIKR	350
HWAR1.AMI	301	LSSSCTIQAY	VTNNILTLWL	QRWVEDSNIQ	ASCMKKK----	-R--SRSSKK	350
RWAR1.AMI	301	LSSSCSIQVY	ITWTLTIVWL	QRWLEDANLH	V-CGRKR----	-R--SRS----	350
			370	380	390	400	
HTRAM.AMI	351	GTENGUNGTL	TSNVADSPRN	KKEKSS.....	.....	.....	400
KIAA0057.AMI	351	ESGYHENGW	KAENGTSPT	KKLKSP.....	.....	.....	400
HWAR1.AMI	351	RTENGV-GVE	TSNRVDCPPK	RKEKSS.....	.....	.....	400
RWAR1.AMI	351	RKGTEN-GVE	NPNRIDSPPK	KKEKAP.....	.....	.....	400



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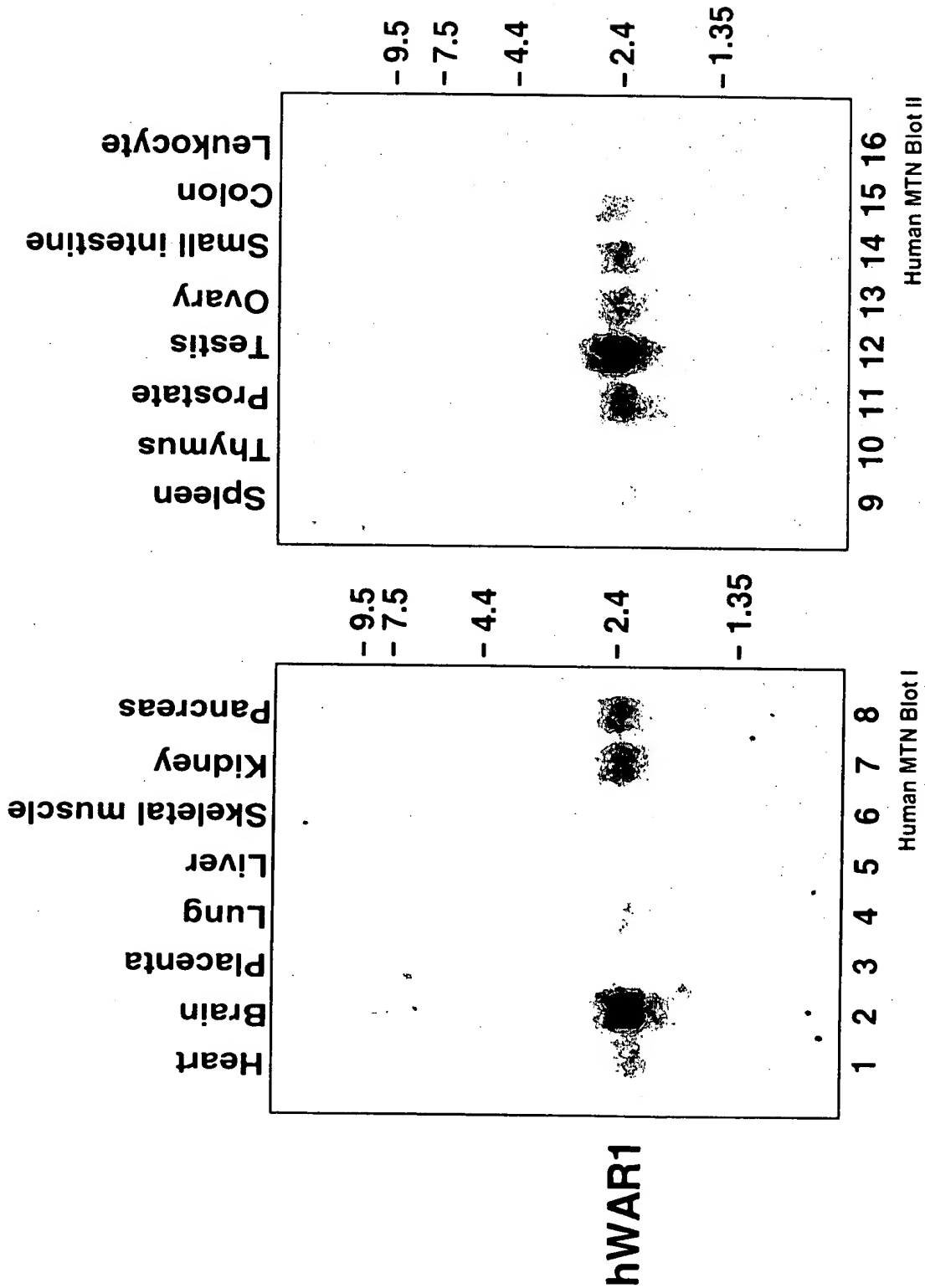
Fig. 3





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Fig. 4

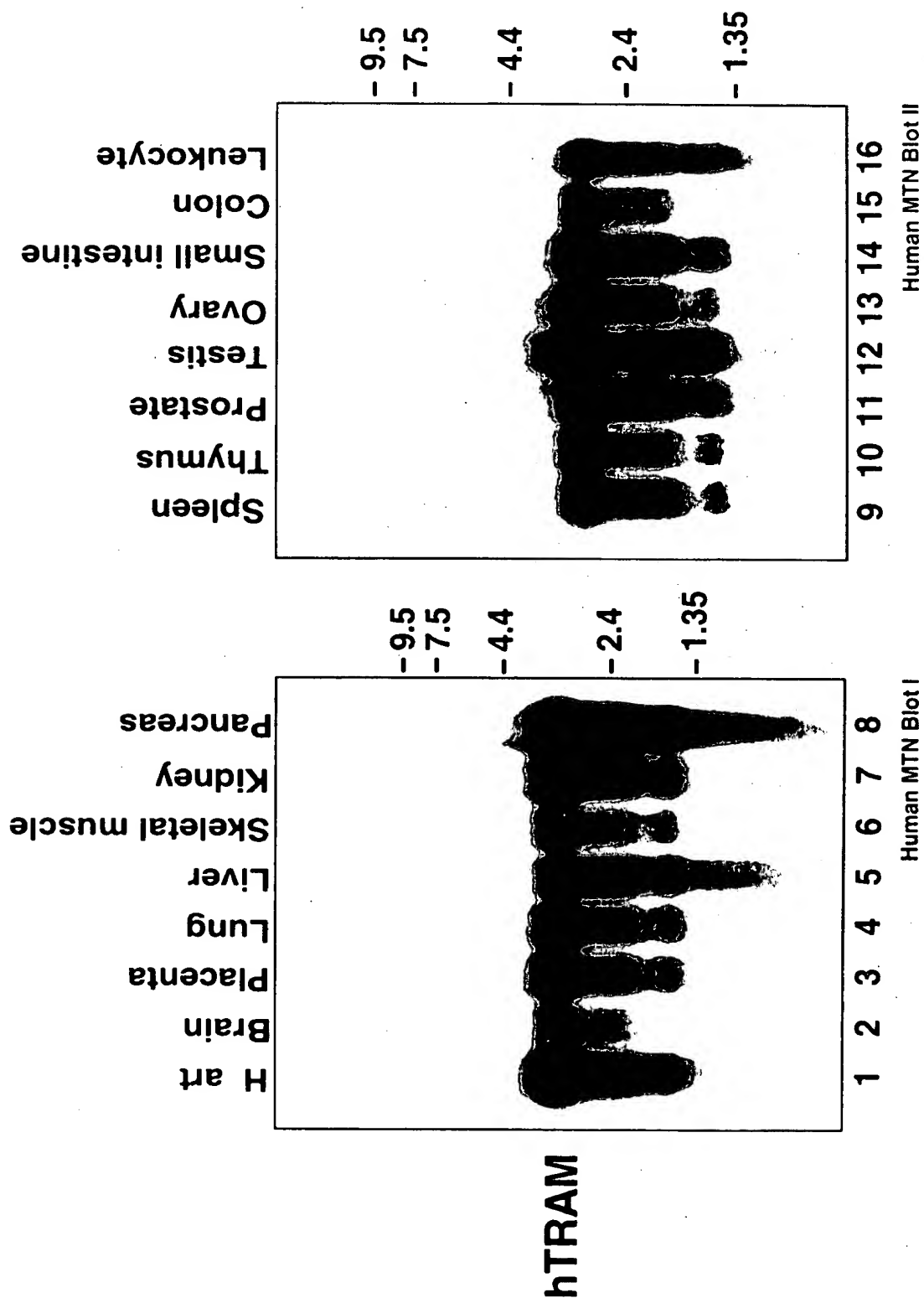






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Fig. 5

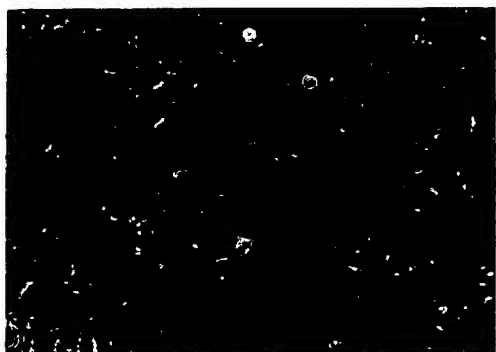




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Fig. 6

A



B



C



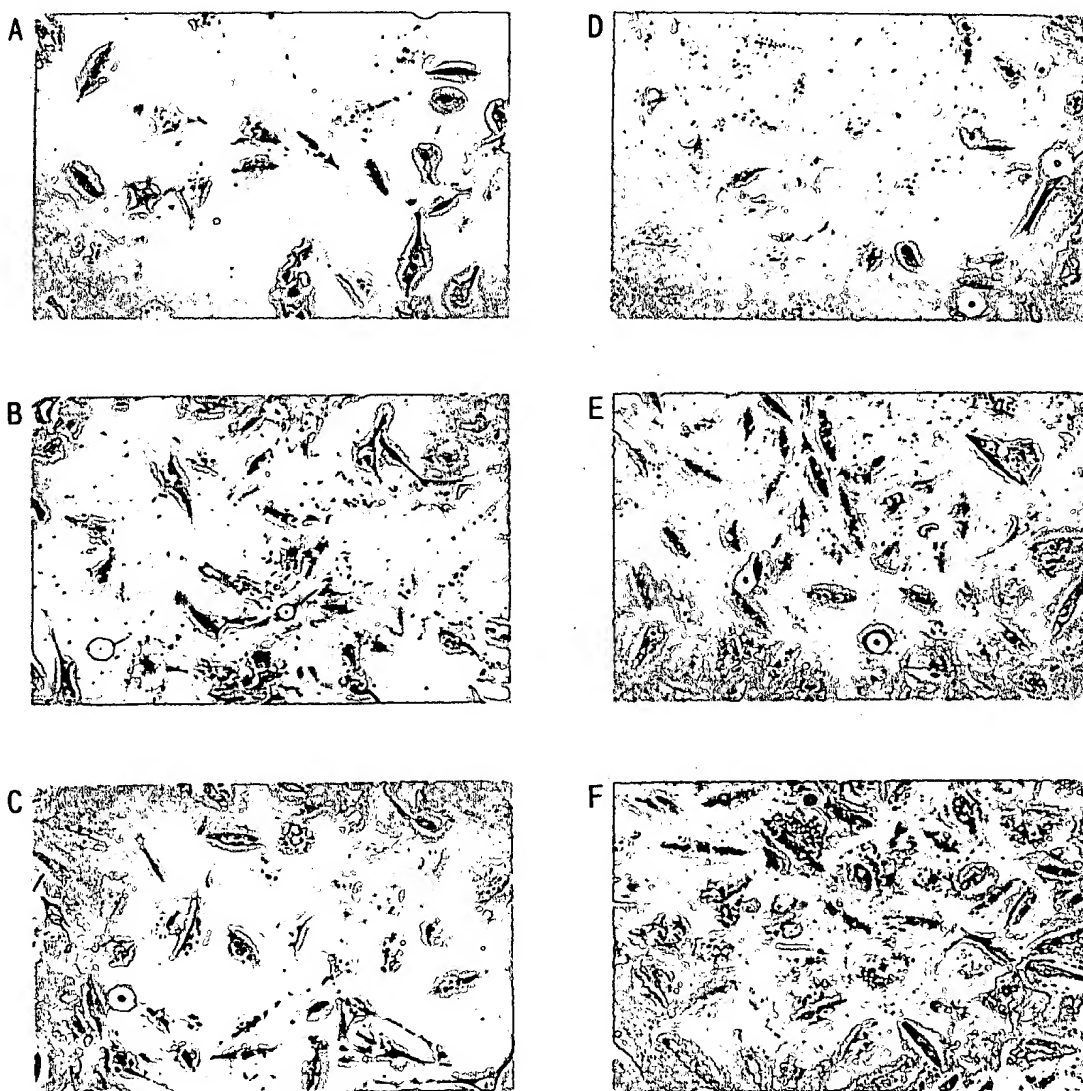
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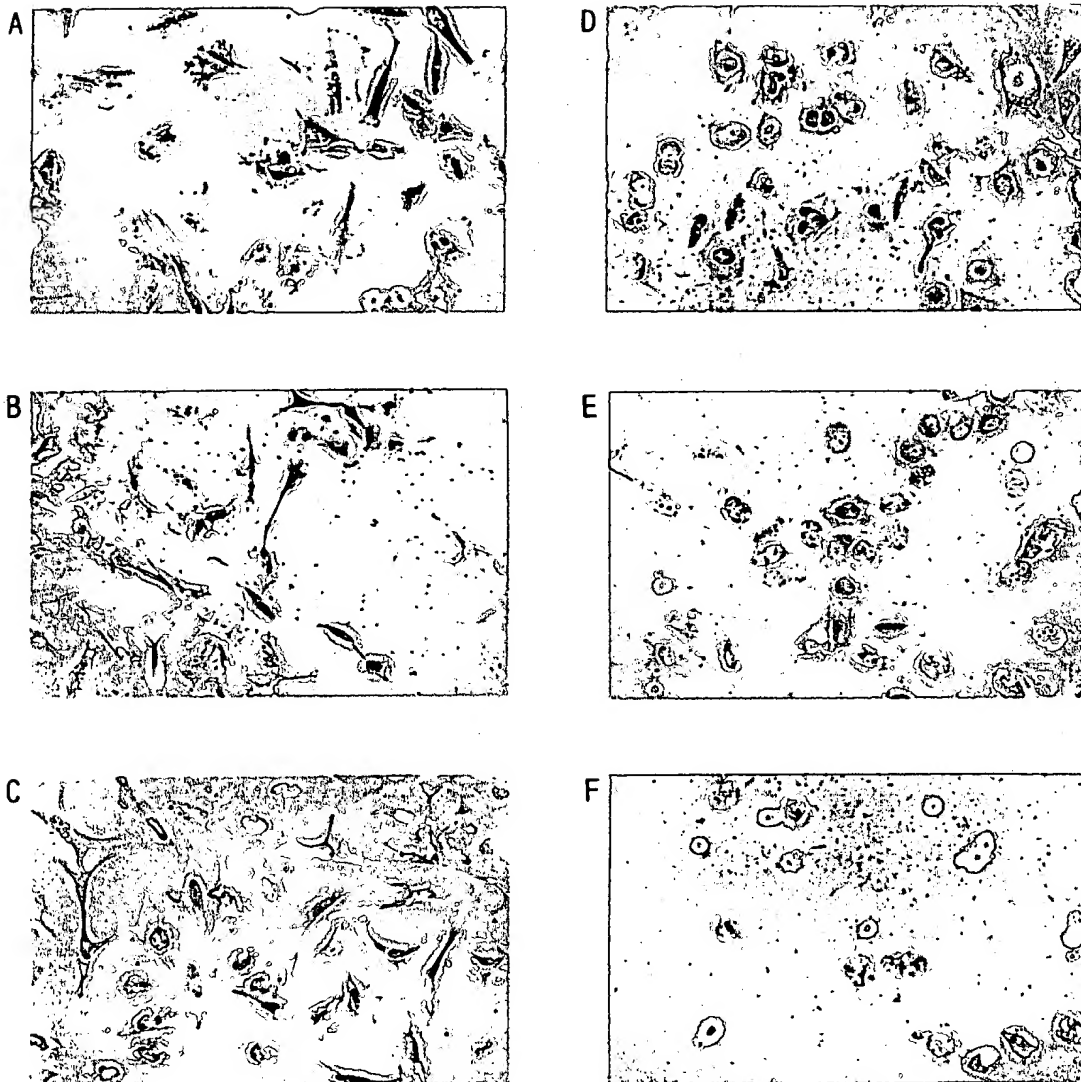
Fig. 7





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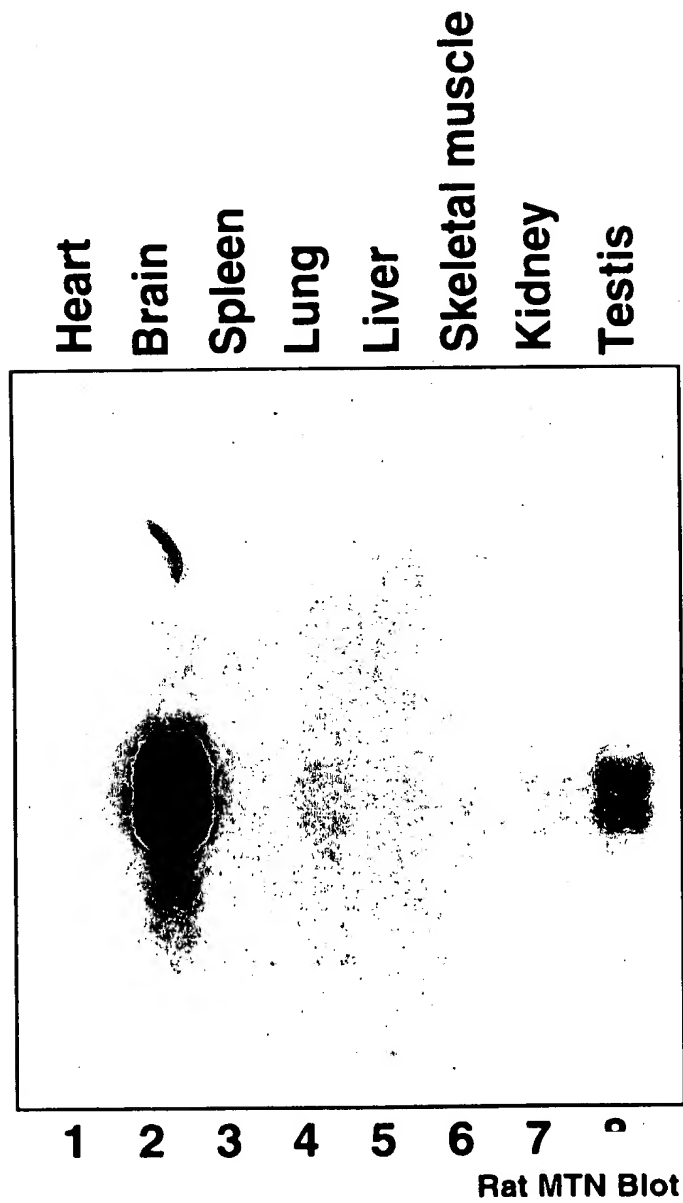
Fig. 8





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Fig. 9





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Fig. 1 0





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Fig. 1 1

